

# SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT EXPRESSED IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF

<130> D0079 NP

<150> US 60/269,535

<151> 2001-02-16

<160> 81

<170> PatentIn version 3.0

<210> 1

<211> 2565

<212> DNA

<213> homo sapiens

<220>  
<221> CDS  
<222> (1)..(1251)

```

<400> 1
atg aca act ctt gtt cct gca acc ctc tcc ttc ctt ctt ctc tgg acc      48
Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr
1          5          10          15

ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc      96
Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val
          20          25          30

aaa tct gga acc aag ggg tcc cag ccc atg tcc ccc tct gat ttc cta     144
Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu
          35          40          45

gac aaa ctt atg ggg cga aca tct gga tat gat gcc agg att cgg ccc     192
Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro
          50          55          60

aat ttt aaa ggc cca ccc gtg aac gtg acc tgc aac atc ttc atc aac     240
Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn
          65          70          75          80

agt ttc agc tcc gtc acc aag acc aca atg gac tac cgg gtg aat gtc     288
Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp Tyr Arg Val Asn Val
          85          90          95

ttc ttg cgg caa cag tgg aat gac cca cgc ctg tcc tac cga gaa tat     336
Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr
          100          105          110

cct gat gac tct ctg gac ctc gat ccc tcc atg ctg gac tct atc tgg     384
Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp
          115          120          125

```

aag cca gac ctc ttc ttt gct aat gag aaa ggg gcc aac ttc cat gag	432
Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu	
130 135 140	
gtg acc acg gac aac aag tta ctg cgc atc ttc aag aat ggg aat gtg	480
Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val	
145 150 155 160	
ctg tac agc atc agg ctg acc ctc att ttg tcc tgc ctg atg gac ctc	528
Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu	
165 170 175	
aag aac ttc ccc atg gac atc cag acc tgc acg atg cag ctt gag agc	576
Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser	
180 185 190	
ttt ggc tac acc atg aaa gac ctc gtg ttt gag tgg ctg gaa gat gct	624
Phe Gly Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala	
195 200 205	
cct gct gtc caa gtg gct gag ggg ctg act ctg ccc cag ttt atc ttg	672
Pro Ala Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu	
210 215 220	
cgg gat gag aag gat cta ggc tgt tgt acc aag cac tac aac aca ggg	720
Arg Asp Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly	
225 230 235 240	
aaa ttc acc tgc atc gag gta aag ttt cac ctg gaa cgg cag atg ggc	768
Lys Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly	
245 250 255	
tac tat ctg att cag atg tac atc ccc agc cta ctc atc gtc atc ctg	816
Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu	
260 265 270	
tcc tgg gtc tcc ttc tgg atc aac atg gat gct gcc cct gcc cgt gtg	864
Ser Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val	
275 280 285	
ggc ctg ggc atc acc acc gtg ctc acc atg acc acc cag agc tct ggc	912
Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly	
290 295 300	
tcc cgg gcc tct ttg cct aag gtg tcc tac gtg aag gca atc gac atc	960
Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile	
305 310 315 320	
tgg atg gct gtg tgt ctg ctc ttt gtg ttc gct gcc ttg ctg gag tat	1008
Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr	
325 330 335	
gct gcc ata aat ttt gtt tct cgt cag cat aaa gaa ttc ata cga ctt	1056
Ala Ala Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu	
340 345 350	

cga aga agg cag agg cgc caa cgc ttg gag gaa gat atc atc caa gaa	1104
Arg Arg Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu	
355 360 365	
agt cgt ttc tat ttc cgt ggc tat ggc ttg ggc cac tgc ctg cag gca	1152
Ser Arg Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala	
370 375 380	
aga gat gga ggt cca atg gaa ggt tct ggc att tat agt ccc caa cct	1200
Arg Asp Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro	
385 390 395 400	
cca gcc cct ctt cta agg gaa gga gaa acc acg cgg aaa ctc tac gtg	1248
Pro Ala Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val	
405 410 415	
gac tgagccaaga gaattgacac catctcccgg gctgtcttcc ctttcacttt	1301
Asp	
cctcatcttc aatatcttct actgggttgt ctataaagtg ctacggtcag aagatatcca	1361
ccagggtctg tgaatagggg gggagctata gagtctgct gctggcctcc tgcttcctcc	1421
tgggtgggct ttctccctca gttagactcc attaggggtt tggacagttc cttcctgac	1481
tcccactcag aacttcaact accagtccca aagctatgtg ggcctatatt gcatggtgcc	1541
aatgggtggct gtacttataa agatggctta tctaccctag tccatatttt ctccatactt	1601
tcccatttct catgagacta aggtttggcc acattcctgg ggccaggatg accttctgcc	1661
cttgctggag cctccctgtt ttccaatact ccagtggaga gtattcagaa cactgctgct	1721
agattctggc atttgtcatc ttaatctgca ccacttctcc ccctgccacc tcccaccag	1781
agcctggcca ttactctgtc ctctgtccct cctgctgcag attcaaatgg tgagtcttc	1841
ctatccacaa gtgctgcct gtggggccta gtcaggtttc cttgaagtga gaggaaggca	1901
aagccgcaag ttccccacct ctcgagaggg ttggaacagt cataggctgc actgggctag	1961
cgactatatg gcccaacaga gaggtgttca agtctcttgg gaagccccac actttgtctt	2021
catccctttt cctattgcgc ttgtctgtc tttcctgttc actgagatac tctcttctgc	2081
tgtctcttag ttttgaggag agcgttctga gctgaccagg gtagctgggt cagaaattac	2141
tgtcagaatt ggggcagaga ctttgggttc tcaaaaagac taaccttcca gatccacctg	2201
aacattctgg tctcagaaat attcgttccg ttccctaatt aactagcatg gtggcaggat	2261
ctgttggaca gctggggagt gtaaaaaaag aaaaatactt gttctttaag aaacttactt	2321
tatgatgcta gaaaactttt gagaaaagtg agatccaagg tagtggaacc caggaggagt	2381
agaatagaga aactattctc agagtgtctt ttgttggtg ggctttcatt tgtttcttct	2441

ttctcaccaa agtctatattt ccagggccct tcatttccaa cctggctctt cacttccttt 2501  
 tgggtgtgcaa ataaagggtgc cgctgcaacc ttgttaagga taataaaaaa aaaaaaaaaa 2561  
 aaaa 2565

<210> 2  
 <211> 417  
 <212> PRT  
 <213> homo sapiens

<400> 2

Met	Thr	Thr	Leu	Val	Pro	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Leu	Trp	Thr	
1				5					10					15		
Leu	Pro	Gly	Gln	Val	Leu	Leu	Arg	Val	Ala	Leu	Ala	Lys	Glu	Glu	Val	
			20					25					30			
Lys	Ser	Gly	Thr	Lys	Gly	Ser	Gln	Pro	Met	Ser	Pro	Ser	Asp	Phe	Leu	
		35					40					45				
Asp	Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp	Ala	Arg	Ile	Arg	Pro	
	50					55					60					
Asn	Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys	Asn	Ile	Phe	Ile	Asn	
	65					70				75					80	
Ser	Phe	Ser	Ser	Val	Thr	Lys	Thr	Thr	Met	Asp	Tyr	Arg	Val	Asn	Val	
				85					90					95		
Phe	Leu	Arg	Gln	Gln	Trp	Asn	Asp	Pro	Arg	Leu	Ser	Tyr	Arg	Glu	Tyr	
			100					105						110		
Pro	Asp	Asp	Ser	Leu	Asp	Leu	Asp	Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp	
		115					120					125				
Lys	Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly	Ala	Asn	Phe	His	Glu	
	130					135					140					
Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe	Lys	Asn	Gly	Asn	Val	
145					150					155					160	
Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Ile	Leu	Ser	Cys	Leu	Met	Asp	Leu	
				165					170					175		

Lys	Asn	Phe	Pro	Met	Asp	Ile	Gln	Thr	Cys	Thr	Met	Gln	Leu	Glu	Ser	180	185	190	
Phe	Gly	Tyr	Thr	Met	Lys	Asp	Leu	Val	Phe	Glu	Trp	Leu	Glu	Asp	Ala	195	200	205	
Pro	Ala	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	210	215	220	
Arg	Asp	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	225	230	235	240
Lys	Phe	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	245	250	255	
Tyr	Tyr	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	260	265	270	
Ser	Trp	Val	Ser	Phe	Trp	Ile	Asn	Met	Asp	Ala	Ala	Pro	Ala	Arg	Val	275	280	285	
Gly	Leu	Gly	Ile	Thr	Thr	Val	Leu	Thr	Met	Thr	Thr	Gln	Ser	Ser	Gly	290	295	300	
Ser	Arg	Ala	Ser	Leu	Pro	Lys	Val	Ser	Tyr	Val	Lys	Ala	Ile	Asp	Ile	305	310	315	320
Trp	Met	Ala	Val	Cys	Leu	Leu	Phe	Val	Phe	Ala	Ala	Leu	Leu	Glu	Tyr	325	330	335	
Ala	Ala	Ile	Asn	Phe	Val	Ser	Arg	Gln	His	Lys	Glu	Phe	Ile	Arg	Leu	340	345	350	
Arg	Arg	Arg	Gln	Arg	Arg	Gln	Arg	Leu	Glu	Glu	Asp	Ile	Ile	Gln	Glu	355	360	365	
Ser	Arg	Phe	Tyr	Phe	Arg	Gly	Tyr	Gly	Leu	Gly	His	Cys	Leu	Gln	Ala	370	375	380	
Arg	Asp	Gly	Gly	Pro	Met	Glu	Gly	Ser	Gly	Ile	Tyr	Ser	Pro	Gln	Pro	385	390	395	400

Pro Ala Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val  
 405 410 415

Asp

<210> 3  
 <211> 1640  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1293)

<400> 3  
 atg aca act ctt gtt cct gca acc ctc tcc ttc ctt ctt ctc tgg acc 48  
 Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr  
 1 5 10 15  
 ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc 96  
 Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val  
 20 25 30  
 aaa tct gga acc aag ggg tcc cag ccc atg tcc ccc tct gat ttc cta 144  
 Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu  
 35 40 45  
 gac aaa ctt atg ggg cga aca tct gga tat gat gcc agg att cgg ccc 192  
 Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro  
 50 55 60  
 aat ttt aaa ggc cca ccc gtg aac gtg acc tgc aac atc ttc atc aac 240  
 Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
 65 70 75 80  
 agt ttc agc tcc gtc acc aag acc aca atg gac tac cgg gtg aat gtc 288  
 Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp Tyr Arg Val Asn Val  
 85 90 95  
 ttc ttg cgg caa cag tgg aat gac cca cgc ctg tcc tac cga gaa tat 336  
 Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr  
 100 105 110  
 cct gat gac tct ctg gac ctc gat ccc tcc atg ctg gac tct atc tgg 384  
 Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp  
 115 120 125  
 aag cca gac ctc ttc ttt gct aat gag aaa ggg gcc aac ttc cat gag 432  
 Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu  
 130 135 140  
 gtg acc acg gac aac aag tta ctg cgc atc ttc aag aat ggg aat gtg 480  
 Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val

145	150	155	160	
ctg tac agc atc agg ctg acc ctc att ttg tcc tgc ctg atg gac ctc				528
Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu	165	170	175	
aag aac ttc ccc atg gac atc cag acg tgc acg atg cag ctt gag agc				576
Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser	180	185	190	
tca tcc ata ctc tgc agc cct ctg cca tct ctg tca ctt tca gtt ggc				624
Ser Ser Ile Leu Cys Ser Pro Leu Pro Ser Leu Ser Leu Ser Val Gly	195	200	205	
tac acc atg aaa gac ctc gtg ttt gag tgg ctg gaa gat gct cct gct				672
Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala Pro Ala	210	215	220	
gtc caa gtg gct gag ggg ctg act ctg ccc cag ttt atc ttg cgg gat				720
Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu Arg Asp	225	230	235	240
gag aag gat cta ggc tgt tgt acc aag cac tac aac aca ggg aaa ttc				768
Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly Lys Phe	245	250	255	
acc tgc atc gag gta aag ttt cac ctg gaa cgg cag atg ggc tac tat				816
Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly Tyr Tyr	260	265	270	
ctg att cag atg tac atc ccc agc cta ctc atc gtc atc ctg tcc tgg				864
Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu Ser Trp	275	280	285	
gtc tcc ttc tgg atc aac atg gat gct gcc cct gcc cgt gtg ggc ctg				912
Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val Gly Leu	290	295	300	
ggc atc acc acc gtg ctc acc atg acc acc cag agc tct ggc tcc cgg				960
Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly Ser Arg	305	310	315	320
gcc tct ttg cct aag gtg tcc tac gtg aag gca atc gac atc tgg atg				1008
Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp Met	325	330	335	
gct gtg tgt ctg ctc ttt gtg ttc gct gcc ttg ctg gag tat gct gcc				1056
Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr Ala Ala	340	345	350	
ata aat ttt gtt tct cgt cag cat aaa gaa ttc ata cga ctt cga aga				1104
Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu Arg Arg	355	360	365	
agg cag agg cgc caa cgc ttg gag gaa gat atc atc caa gaa agt cgt				1152
Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu Ser Arg	370	375	380	

ttc tat ttc cgt ggc tat ggc ttg ggc cac tgc ctg cag gca aga gat	1200
Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala Arg Asp	
385 390 395 400	
gga ggt cca atg gaa ggt tct ggc att tat agt ccc caa cct cca gcc	1248
Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro Pro Ala	
405 410 415	
cct ctt cta agg gaa gga gaa acc acg cgg aaa ctc tac gtg gac	1293
Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp	
420 425 430	
tgagccaaga gaattgacac catctcccgg gctgtcttcc ctttcacttt cctcatcttc	1353
aatatcttct actggggttg ctataaagt ctatggtcag aagatatcca ccaggctctg	1413
tgaatagggt gggagctata gagtcttgct gctggcctcc tgcttctctcc tgggtgggct	1473
ttctccctca gttagaactcc attaggggtt tggacagttc cttctctgac tcccactcag	1533
aacttcaact accagtccca aagctatgtg ggcctatatt gcatgggtgcc aatgggtggct	1593
gtacttataa agatggotta tctaccctaa aaaaaaaaaa aaaaaaa	1640
<210> 4	
<211> 431	
<212> PRT	
<213> homo sapiens	
<400> 4	
Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr	
1 5 10 15	
Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val	
20 25 30	
Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu	
35 40 45	
Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro	
50 55 60	
Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn	
65 70 75 80	
Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp Tyr Arg Val Asn Val	
85 90 95	





325

330

335

Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr Ala Ala  
340 345 350

Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu Arg Arg  
355 360 365

Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu Ser Arg  
370 375 380

Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala Arg Asp  
385 390 395 400

Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro Pro Ala  
405 410 415

Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
420 425 430

<210> 5

<211> 679

<212> DNA

<213> homo sapiens

<400> 5

atatagcacg tagagctgct tagcatacat ctatctcatg agtagtggtg tgaccataaa 60  
aagcatgcaa tgggcctgtg tacccaaggc acctgtctg cataacattc cctatgagat 120  
attgatgggt ggtctgttct ctatccctct gcctttgagc ttgacctca aattctgccg 180  
tttcttcctt gtaattccag gaggaagata tcatccaaga aagtcgtttc tatttccgtg 240  
gctatggctt gggccactgc ctgcaggcaa gagatggagg tccaatggaa ggttctggca 300  
tttatagtcc ccaacctcca gccoctcttc taagggaagg agaaaccacg cggaaactct 360  
acgtggactg agccaagaga attgacacca tctcccgggc tgtcttcctt ttcactttcc 420  
tcatcttcaa tatcttctac tgggttgtct ataaagtgct atggtcagaa gatatccacc 480  
aggctctgtg aatagggtgg gagctataga gtccctgtgc tggcctcctg cttcctcctg 540  
gggtgggctt ctccctcagt tagactccat taggggtttg gacagttcct tctgatctc 600  
ccactcagaa cttcaactac cagtcccaaa gctatgtggg cctatattgc atggtgccaa 660  
tggtggctgt acttataaa 679

```

<210> 6
<211> 80
<212> DNA
<213> homo sapiens

<400> 6
aggggctgga ggttggggac tataaatgcc agaaccttcc attggacctc catctcttgc      60

ctgcaggcag tggcccaagc                                         80

<210> 7
<211> 20
<212> DNA
<213> homo sapiens

<400> 7
tcgtttctat ttccgtggct                                         20

<210> 8
<211> 20
<212> DNA
<213> homo sapiens

<400> 8
cgggagatgg tgtcaattct                                         20

<210> 9
<211> 993
<212> DNA
<213> homo sapiens

<400> 9
atgacaactc ttgttctctgc aacctctctc ttccttcttc tctggacctc gccagggcag      60

gtcctcctca ggggtggcctt ggcaaaagag gaagtcaaat ctggaaccaa ggggtcccag      120

cccatgtccc cctctgattt cctagacaaa cttatggggc gaacatctgg atatgatgcc      180

aggattcggc ccaattttta aggccccacc gtgaacgtga cctgcaacat cttcatcaac      240

agtttcagct ccatacacia gaccacaatg gcttgctggg ccctggggaa tggcaatggt      300

tctgaagggc ccatactctgc accctcccag gactaccggg tgaatgtctt cttgcggcaa      360

cagtggaatg acccagcctt gtcctaccga gaatatcttg atgactctct ggacctcgat      420

ccctccatgc tggactctat ctggaagcca gacctcttct ttgctaataa gaaagggggc      480

aacttccatg aggtgaccac ggacaacaag ttactgcgca tcttcaagaa tgggaatgtg      540

ctgtacagca tcaggctgac cctcattttg tcctgcctga tggacctcaa gaacttcccc      600

atggacatcc agacctgcac gatgcagctt gagagctttg gctacaccat gaaagacctc      660

```

gtgtttgagt ggctggaaga tgctcctgct gtccaagtgg ctgaggggct gactctgccc 720  
cagtttatct tgcgggatga gaaggatcta ggctgttgta ccaagcacta caacacaggg 780  
aaattcacct gcatcgaggt aaagtttcac ctggaacggc agatgggcta ctatctgatt 840  
cagatgtaca tccccagcct actcatcgtc atcctgtcct gggctctcctt ctggatcaac 900  
atggatgctg cccctgcccg tgtgggcctg ggcatcacca ccgtgctcac catgaccacc 960  
cagagctctg gctcccgggc ctctttgcct aag 993

<210> 10  
<211> 449  
<212> PRT  
<213> Homo sapiens

<400> 10

Met	Tyr	Ser	Phe	Asn	Thr	Leu	Arg	Leu	Tyr	Leu	Ser	Gly	Ala	Ile	Val	1	5	10	15
Phe	Phe	Ser	Leu	Ala	Ala	Ser	Lys	Glu	Ala	Glu	Ala	Ala	Arg	Ser	Ala	20	25	30	
Thr	Lys	Pro	Met	Ser	Pro	Ser	Asp	Phe	Leu	Asp	Lys	Leu	Met	Gly	Arg	35	40	45	
Thr	Ser	Gly	Tyr	Asp	Ala	Arg	Ile	Arg	Pro	Asn	Phe	Lys	Gly	Pro	Pro	50	55	60	
Val	Asn	Val	Ser	Cys	Asn	Ile	Phe	Ile	Asn	Ser	Phe	Gly	Ser	Ile	Ala	65	70	75	80
Glu	Thr	Thr	Met	Asp	Tyr	Arg	Val	Asn	Ile	Phe	Leu	Arg	Gln	Gln	Trp	85	90	95	
Asn	Asp	Pro	Arg	Leu	Ala	Tyr	Asn	Glu	Tyr	Pro	Asp	Asp	Ser	Leu	Asp	100	105	110	
Leu	Asp	Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp	Lys	Pro	Asp	Leu	Phe	Phe	115	120	125	
Ala	Asn	Glu	Lys	Gly	Ala	His	Phe	His	Glu	Ile	Thr	Thr	Asp	Asn	Lys	130	135	140	
Leu	Leu	Arg	Ile	Ser	Arg	Asn	Gly	Asn	Val	Leu	Tyr	Ser	Ile	Arg	Ile	145	150	155	160
Thr	Leu	Thr	Leu	Ala	Cys	Pro	Met	Asp	Leu	Lys	Asn	Phe	Pro	Met	Asp	165	170	175	
Val	Gln	Thr	Cys	Ile	Met	Gln	Leu	Glu	Ser	Phe	Gly	Tyr	Thr	Met	Asn	180	185	190	

Asp	Leu	Ile	Phe	Glu	Trp	Gln	Glu	Gln	Gly	Ala	Val	Gln	Val	Ala	Asp
	195						200					205			
Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	Lys	Glu	Glu	Lys	Asp	Leu	Arg
	210					215					220				
Tyr	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	Lys	Phe	Thr	Cys	Ile	Glu	Ala
225					230					235					240
Arg	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	Tyr	Tyr	Leu	Ile	Gln	Met	Tyr
				245					250					255	
Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	Ser	Trp	Ile	Ser	Phe	Trp	Ile
			260					265						270	
Asn	Met	Asp	Ala	Ala	Pro	Ala	Arg	Val	Gly	Leu	Gly	Ile	Thr	Thr	Val
		275					280					285			
Leu	Thr	Met	Thr	Thr	Gln	Ser	Ser	Gly	Ser	Arg	Ala	Ser	Leu	Pro	Lys
	290					295					300				
Val	Ser	Tyr	Val	Lys	Ala	Ile	Asp	Ile	Trp	Met	Ala	Val	Cys	Leu	Leu
305					310					315					320
Phe	Val	Phe	Ser	Ala	Leu	Leu	Glu	Tyr	Ala	Ala	Val	Asn	Phe	Val	Ser
				325					330					335	
Arg	Gln	His	Lys	Glu	Leu	Leu	Arg	Phe	Arg	Arg	Lys	Arg	Arg	His	His
			340					345					350		
Lys	Glu	Asp	Glu	Ala	Gly	Glu	Gly	Arg	Phe	Asn	Phe	Ser	Ala	Tyr	Gly
		355					360					365			
Met	Gly	Pro	Ala	Cys	Leu	Gln	Ala	Lys	Asp	Gly	Ile	Ser	Val	Lys	Gly
	370					375					380				
Ala	Asn	Asn	Ser	Asn	Thr	Thr	Asn	Pro	Pro	Pro	Ala	Pro	Ser	Lys	Ser
385					390					395					400
Pro	Glu	Glu	Met	Arg	Lys	Leu	Phe	Ile	Gln	Arg	Ala	Lys	Lys	Ile	Asp
				405					410					415	
Lys	Ile	Ser	Arg	Ile	Gly	Phe	Pro	Met	Ala	Phe	Leu	Ile	Phe	Asn	Met
			420					425					430		
Phe	Tyr	Trp	Ile	Ile	Tyr	Lys	Ile	Val	Arg	Arg	Glu	Asp	Val	His	Asn
	435						440					445			

Gln

<210> 11  
 <211> 465  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 11

Met	Ala	His	Val	Arg	His	Phe	Arg	Thr	Leu	Val	Ser	Gly	Phe	Tyr	Phe	1	5	10	15
Trp	Glu	Ala	Ala	Leu	Leu	Leu	Ser	Leu	Val	Ala	Thr	Lys	Glu	Thr	Asp	20	25	30	
Ser	Ala	Arg	Ser	Arg	Ser	Ala	Pro	Met	Ser	Pro	Ser	Asp	Phe	Leu	Asp	35	40	45	
Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp	Ala	Arg	Ile	Arg	Pro	Asn	50	55	60	
Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys	Asn	Ile	Phe	Ile	Asn	Ser	65	70	75	
Phe	Gly	Ser	Ile	Ala	Glu	Thr	Thr	Met	Asp	Tyr	Arg	Val	Asn	Ile	Phe	85	90	95	
Leu	Arg	Gln	Lys	Trp	Asn	Asp	Pro	Arg	Leu	Ala	Tyr	Ser	Glu	Tyr	Pro	100	105	110	
Asp	Asp	Ser	Leu	Asp	Leu	Asp	Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp	Lys	115	120	125	
Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly	Ala	Asn	Phe	His	Glu	Val	130	135	140	
Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe	Lys	Asn	Gly	Asn	Val	Leu	145	150	155	
Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Thr	Leu	Ser	Cys	Pro	Met	Asp	Leu	Lys	165	170	175	
Asn	Phe	Pro	Met	Asp	Val	Gln	Thr	Cys	Ile	Met	Gln	Leu	Glu	Ser	Phe	180	185	190	
Gly	Tyr	Thr	Met	Asn	Asp	Leu	Ile	Phe	Glu	Trp	Gln	Asp	Glu	Ala	Pro	195	200	205	
Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Leu	Leu	Lys	Glu	210	215	220	
Glu	Lys	Asp	Leu	Arg	Tyr	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	Lys	Phe	225	230	235	
Thr	Cys	Ile	Glu	Val	Arg	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	Tyr	Tyr	245	250	255	
Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	Ser	Trp	260	265	270	
Val	Ser	Phe	Trp	Ile	Asn	Met	Asp	Ala	Ala	Pro	Ala	Arg	Val	Ala	Leu	275	280	285	
Gly	Ile	Thr	Thr	Val	Leu	Thr	Met	Thr	Thr	Gln	Ser	Ser	Gly	Ser	Arg	290	295	300	

```

Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp Met
305                      310                      315                      320

Ala Val Cys Leu Leu Phe Val Phe Ser Ala Leu Leu Glu Tyr Ala Ala
                      325                      330                      335

Val Asn Phe Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg
                      340                      345                      350

Lys Arg Lys Asn Lys Thr Glu Ala Phe Ala Leu Glu Lys Phe Tyr Arg
                      355                      360                      365

Phe Ser Asp Met Asp Asp Glu Val Arg Glu Ser Arg Phe Ser Phe Thr
                      370                      375                      380

Ala Tyr Gly Met Gly Pro Cys Leu Gln Ala Lys Asp Gly Met Thr Pro
385                      390                      395                      400

Lys Gly Pro Asn His Pro Val Gln Val Met Pro Lys Ser Pro Asp Glu
                      405                      410                      415

Met Arg Lys Val Phe Ile Asp Arg Ala Lys Lys Ile Asp Thr Ile Ser
420                      425                      430

Arg Ala Cys Phe Pro Leu Ala Phe Leu Ile Phe Asn Ile Phe Tyr Trp
435                      440                      445

Val Ile Tyr Lys Ile Leu Arg His Glu Asp Ile His His Gln Gln Gln
450                      455                      460

Asp
465

<210> 12
<211> 337
<212> PRT
<213> Mus musculus

<220>
<221> UNSURE
<222> (322)..(322)
<223> wherein "X" is any amino acid.

<400> 12

Val Ala Leu Ala Lys Glu Asp Val Lys Ser Gly Leu Lys Gly Ser Gln
1                      5                      10                      15

Pro Met Ser Pro Ser Asp Phe Leu Asp Lys Leu Met Gly Arg Thr Ser
20                      25                      30

Gly Tyr Asp Ala Arg Ile Arg Pro Asn Phe Lys Gly Pro Pro Val Asn
35                      40                      45

Val Thr Cys Asn Ile Phe Ile Asn Ser Phe Gly Ser Val Thr Glu Thr

```

50

55

60

Thr Met Asp Tyr Arg Val Asn Val Phe Leu Arg Gln Gln Trp Asn Asp  
65 70 75 80

Pro Arg Leu Ala Tyr Arg Glu Tyr Pro Asp Asp Ser Leu Asp Leu Asp  
85 90 95

Pro Ser Met Leu Asp Ser Ile Trp Lys Pro Asp Leu Phe Phe Ala Asn  
100 105 110

Glu Lys Gly Ala Asn Phe His Glu Val Thr Thr Asp Asn Lys Leu Leu  
115 120 125

Arg Ile Phe Lys Asn Gly Asn Val Leu Tyr Ser Ile Arg Leu Thr Leu  
130 135 140

Ile Leu Ser Cys Pro Met Asp Leu Lys Asn Phe Pro Met Asp Ile Gln  
145 150 155 160

Thr Cys Thr Met Gln Leu Glu Ser Phe Gly Tyr Thr Met Asn Asp Leu  
165 170 175

Met Phe Glu Trp Leu Glu Asp Ala Pro Ala Val Gln Val Ala Glu Gly  
180 185 190

Leu Thr Leu Pro Gln Phe Ile Leu Arg Asp Glu Lys Asp Leu Gly Tyr  
195 200 205

Cys Thr Lys His Tyr Asn Thr Gly Lys Phe Thr Cys Ile Glu Val Lys  
210 215 220

Phe His Leu Glu Arg Gln Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile  
225 230 235 240

Pro Ser Leu Leu Ile Val Ile Leu Ser Trp Val Ser Phe Trp Ile Asn  
245 250 255

Met Asp Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu  
260 265 270

Thr Met Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val  
275 280 285

Ser Tyr Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe  
290 295 300

Val Phe Ala Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg  
305 310 315 320

Gln Xaa Lys Glu Phe Met Arg Leu Arg Arg Arg Gln Arg Arg Gln Arg  
325 330 335

Met

&lt;210&gt; 13



<211> 452  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Met	Asn	Arg	Gln	Leu	Val	Asn	Ile	Leu	Thr	Ala	Leu	Phe	Ala	Phe	Phe	
1				5					10					15		
Leu	Glu	Thr	Asn	His	Phe	Arg	Thr	Ala	Phe	Cys	Lys	Asp	His	Asp	Ser	
			20					25					30			
Arg	Ser	Gly	Lys	Gln	Pro	Ser	Gln	Thr	Leu	Ser	Pro	Ser	Asp	Phe	Leu	
		35					40					45				
Asp	Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp	Ala	Arg	Ile	Arg	Pro	
	50					55					60					
Asn	Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys	Asn	Ile	Phe	Ile	Asn	
65					70					75					80	
Ser	Phe	Gly	Ser	Val	Thr	Glu	Thr	Thr	Met	Asp	Tyr	Arg	Val	Asn	Ile	
				85					90					95		
Phe	Leu	Arg	Gln	Gln	Trp	Asn	Asp	Ser	Arg	Leu	Ala	Tyr	Ser	Glu	Tyr	
			100					105					110			
Pro	Asp	Asp	Ser	Leu	Asp	Leu	Asp	Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp	
		115					120					125				
Lys	Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly	Ala	Asn	Phe	His	Asp	
	130					135					140					
Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Ser	Lys	Asn	Gly	Lys	Val	
145					150					155					160	
Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Thr	Leu	Ser	Cys	Pro	Met	Asp	Leu	
				165					170					175		
Lys	Asn	Phe	Pro	Met	Asp	Val	Gln	Thr	Cys	Thr	Met	Gln	Leu	Glu	Ser	
			180					185					190			
Phe	Gly	Tyr	Thr	Met	Asn	Asp	Leu	Ile	Phe	Glu	Trp	Leu	Ser	Asp	Gly	
		195					200					205				
Pro	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	Lys	
	210					215					220					
Glu	Glu	Lys	Glu	Leu	Gly	Tyr	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	Lys	
225					230					235					240	
Phe	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	Tyr	
				245					250					255		
Tyr	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	Ser	
			260					265					270			

Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val Ala  
 275 280 285  
 Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly Ser  
 290 295 300  
 Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp  
 305 310 315 320  
 Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr Ala  
 325 330 335  
 Ala Val Asn Phe Val Ser Arg Gln His Lys Glu Phe Leu Arg Leu Arg  
 340 345 350  
 Arg Arg Gln Lys Arg Gln Asn Lys Glu Glu Asp Val Thr Arg Glu Ser  
 355 360 365  
 Arg Phe Asn Phe Ser Gly Tyr Gly Met Gly His Cys Leu Gln Val Lys  
 370 375 380  
 Asp Gly Thr Ala Val Lys Ala Thr Pro Ala Asn Pro Leu Pro Gln Pro  
 385 390 395 400  
 Pro Lys Asp Gly Asp Ala Ile Lys Lys Lys Phe Val Asp Arg Ala Lys  
 405 410 415  
 Arg Ile Asp Thr Ile Ser Arg Ala Ala Phe Pro Leu Ala Phe Leu Ile  
 420 425 430  
 Phe Asn Ile Phe Tyr Trp Ile Thr Tyr Lys Ile Ile Arg His Glu Asp  
 435 440 445  
 Val His Lys Lys  
 450  
 <210> 14  
 <211> 298  
 <212> PRT  
 <213> homo sapiens  
 <400> 14

Pro Ser Asp Phe Leu Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp  
 1 5 10 15  
 Ala Arg Ile Arg Pro Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys  
 20 25 30  
 Asn Ile Phe Ile Asn Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp  
 35 40 45  
 Tyr Arg Val Asn Val Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu  
 50 55 60  
 Ser Tyr Arg Glu Tyr Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met  
 65 70 75 80

Leu	Asp	Ser	Ile	Trp	Lys	Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly		
				85					90					95			
Ala	Asn	Phe	His	Glu	Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe		
			100					105					110				
Lys	Asn	Gly	Asn	Val	Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Ile	Leu	Ser		
		115					120					125					
Cys	Leu	Met	Asp	Leu	Lys	Asn	Phe	Pro	Met	Asp	Ile	Gln	Thr	Cys	Thr		
	130					135					140						
Met	Gln	Leu	Glu	Ser	Phe	Gly	Tyr	Thr	Met	Lys	Asp	Leu	Val	Phe	Glu		
145					150					155					160		
Trp	Leu	Glu	Asp	Ala	Pro	Ala	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu		
				165				170							175		
Pro	Gln	Phe	Ile	Leu	Arg	Asp	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys		
			180					185					190				
His	Tyr	Asn	Thr	Gly	Lys	Phe	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu		
		195					200					205					
Glu	Arg	Gln	Met	Gly	Tyr	Tyr	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu		
	210					215					220						
Leu	Ile	Val	Ile	Leu	Ser	Trp	Val	Ser	Phe	Trp	Ile	Asn	Met	Asp	Ala		
225					230					235					240		
Ala	Pro	Ala	Arg	Val	Gly	Leu	Gly	Ile	Thr	Thr	Val	Leu	Thr	Met	Thr		
				245					250					255			
Thr	Gln	Ser	Ser	Gly	Ser	Arg	Ala	Ser	Leu	Pro	Lys	Val	Ser	Tyr	Val		
			260				265						270				
Lys	Ala	Ile	Asp	Ile	Trp	Met	Ala	Val	Cys	Leu	Leu	Phe	Val	Phe	Ala		
		275				280						285					
Ala	Leu	Leu	Glu	Tyr	Ala	Ala	Ile	Asn	Phe								
	290					295											

<210> 15  
 <211> 312  
 <212> PRT  
 <213> homo sapiens

<400> 15

Pro	Ser	Asp	Phe	Leu	Asp	Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp		
1				5					10					15			
Ala	Arg	Ile	Arg	Pro	Asn	Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys		
			20					25					30				
Asn	Ile	Phe	Ile	Asn	Ser	Phe	Ser	Ser	Val	Thr	Lys	Thr	Thr	Met	Asp		

35					40					45					
Tyr	Arg	Val	Asn	Val	Phe	Leu	Arg	Gln	Gln	Trp	Asn	Asp	Pro	Arg	Leu
50						55					60				
Ser	Tyr	Arg	Glu	Tyr	Pro	Asp	Asp	Ser	Leu	Asp	Leu	Asp	Pro	Ser	Met
65					70					75					80
Leu	Asp	Ser	Ile	Trp	Lys	Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly
			85						90					95	
Ala	Asn	Phe	His	Glu	Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe
			100					105					110		
Lys	Asn	Gly	Asn	Val	Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Ile	Leu	Ser
		115					120					125			
Cys	Leu	Met	Asp	Leu	Lys	Asn	Phe	Pro	Met	Asp	Ile	Gln	Thr	Cys	Thr
	130					135					140				
Met	Gln	Leu	Glu	Ser	Ser	Ser	Ile	Leu	Cys	Ser	Pro	Leu	Pro	Ser	Leu
145						150				155					160
Ser	Leu	Ser	Val	Gly	Tyr	Thr	Met	Lys	Asp	Leu	Val	Phe	Glu	Trp	Leu
				165					170					175	
Glu	Asp	Ala	Pro	Ala	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln
			180					185					190		
Phe	Ile	Leu	Arg	Asp	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys	His	Tyr
		195					200					205			
Asn	Thr	Gly	Lys	Phe	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg
	210					215					220				
Gln	Met	Gly	Tyr	Tyr	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile
225					230					235					240
Val	Ile	Leu	Ser	Trp	Val	Ser	Phe	Trp	Ile	Asn	Met	Asp	Ala	Ala	Pro
				245					250					255	
Ala	Arg	Val	Gly	Leu	Gly	Ile	Thr	Thr	Val	Leu	Thr	Met	Thr	Thr	Gln
			260					265					270		
Ser	Ser	Gly	Ser	Arg	Ala	Ser	Leu	Pro	Lys	Val	Ser	Tyr	Val	Lys	Ala
		275					280					285			
Ile	Asp	Ile	Trp	Met	Ala	Val	Cys	Leu	Leu	Phe	Val	Phe	Ala	Ala	Leu
	290					295					300				
Leu	Glu	Tyr	Ala	Ala	Ile	Asn	Phe								
305					310										

<210> 16  
 <211> 13  
 <212> PRT  
 <213> homo sapiens

<400> 16

Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr Pro Asp Asp  
1 5 10

<210> 17

<211> 13

<212> PRT

<213> homo sapiens

<400> 17

Gly Asn Val Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu  
1 5 10

<210> 18

<211> 13

<212> PRT

<213> homo sapiens

<400> 18

Glu Ser Phe Gly Tyr Thr Met Lys Asp Leu Val Phe Glu  
1 5 10

<210> 19

<211> 13

<212> PRT

<213> homo sapiens

<400> 19

Thr Lys His Tyr Asn Thr Gly Lys Phe Thr Cys Ile Glu  
1 5 10

<210> 20

<211> 13

<212> PRT

<213> homo sapiens

<400> 20

Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
1 5 10

<210> 21

<211> 12

<212> PRT

<213> homo sapiens

<400> 21

Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
1 5 10

<210> 22

<211> 14  
<212> PRT  
<213> homo sapiens

<400> 22

Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
1 5 10

<210> 23  
<211> 27  
<212> PRT  
<213> homo sapiens

<400> 23

Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val  
1 5 10 15

Ile Leu Ser Trp Val Ser Phe Trp Ile Asn Met  
20 25

<210> 24  
<211> 18  
<212> PRT  
<213> homo sapiens

<400> 24

Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser  
1 5 10 15

Gly Ser

<210> 25  
<211> 24  
<212> PRT  
<213> homo sapiens

<400> 25

Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu  
1 5 10 15

Tyr Ala Ala Ile Asn Phe Val Ser  
20

<210> 26  
<211> 27  
<212> PRT  
<213> homo sapiens

<400> 26

Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val  
1 5 10 15

Ile Leu Ser Trp Val Ser Phe Trp Ile Asn Met  
20 25

<210> 27  
<211> 18  
<212> PRT  
<213> homo sapiens

<400> 27

Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser  
1 5 10 15

Gly Ser

<210> 28  
<211> 24  
<212> PRT  
<213> homo sapiens

<400> 28

Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu  
1 5 10 15

Tyr Ala Ala Ile Asn Phe Val Ser  
20

<210> 29  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 29

Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
1 5 10

<210> 30  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 30

Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr Pro Asp Asp  
1 5 10

<210> 31  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 31

Gly Asn Val Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu  
1 5 10

<210> 32  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 32

Leu Ser Val Gly Tyr Thr Met Lys Asp Leu Val Phe Glu  
1 5 10

<210> 33  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 33

Thr Lys His Tyr Asn Thr Gly Lys Phe Thr Cys Ile Glu  
1 5 10

<210> 34  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 34

Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
1 5 10

<210> 35  
<211> 12  
<212> PRT  
<213> homo sapiens

<400> 35

Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
1 5 10

<210> 36  
<211> 8  
<212> PRT  
<213> bacteriophage T7

<400> 36

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 37  
<211> 733  
<212> DNA  
<213> homo sapiens



```

<400> 37
gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg      60

aatlcgaggg tgcaccgtca gtcttcctct tcccccaaa acccaaggac accctcatga      120

tctcccgga tctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg      180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg      240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact      300

ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctocca acccccatcg      360

agaaaacat ctcaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc      420

catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct      480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga      540

ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctcaccgtgg      600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc      660

acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc      720

gactctagag gat      733

<210> 38
<211> 23
<212> DNA
<213> Homo sapiens

<400> 38
caggtgcagc tgggtgcagtc tgg      23

<210> 39
<211> 23
<212> DNA
<213> Homo sapiens

<400> 39
caggtcaact taaggagtc tgg      23

<210> 40
<211> 23
<212> DNA
<213> Homo sapiens

<400> 40
gaggtgcagc tgggtggagtc tgg      23

<210> 41

```

<211> 23  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 41  
 caggtgcagc tgcaggagtc ggg 23  
  
 <210> 42  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 42  
 gaggtgcagc tggtgcagtc tgc 23  
  
 <210> 43  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens  
 <400> 43 23  
 caggtacagc tgcagcagtc agg  
 <210> 44  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 44 24  
 tgaggagacg gtgaccaggg tgcc  
 <210> 45  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 45 24  
 tgaagagacg gtgaccattg tccc  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 46 24  
 tgaggagacg gtgaccaggg ttcc  
  
 <210> 47  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens

<400> 47	
tgaggagacg gtgaccgtgg tccc	24
<210> 48	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 48	
gacatccaga tgacccagtc tcc	23
<210> 49	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 49	
gatgttgtga tgactcagtc tcc	23
<210> 50	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 50	
gatattgtga tgactcagtc tcc	23
<210> 51	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 51	
gaaattgtgt tgacgcagtc tcc	23
<210> 52	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 52	
gacatcgtga tgacccagtc tcc	23
<210> 53	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 53	
gaaacgacac tcacgcagtc tcc	23

<210> 54  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 54  
gaaattgtgc tgactcagtc tcc

23

<210> 55  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 55  
cagtctgtgt tgacgcagcc gcc

23

<210> 56  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 56  
cagtctgccc tgactcagcc tgc

23

<210> 57  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 57  
tcctatgtgc tgactcagcc acc

23

<210> 58  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 58  
tcttctgagc tgactcagga ccc

23

<210> 59  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 59  
cacgttatac tgactcaacc gcc

23

<210> 60

<211> 23  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 60  
 caggctgtgc tcactcagcc gtc 23  
  
 <210> 61  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 61  
 aattttatgc tgactcagcc cca 23  
  
 <210> 62  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 62  
 acgtttgatt tccaccttgg tccc 24  
 <210> 63  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 63  
 acgtttgatc tccagcttgg tccc 24  
 <210> 64  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 64  
 acgtttgata tccactttgg tccc 24  
  
 <210> 65  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
 <400> 65  
 acgtttgatc tccaccttgg tccc 24  
  
 <210> 66  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens

<400> 66	
acgtttaatc tccagtcgtg tccc	24
<210> 67	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 67	
cagtctgtgt tgacgcagcc gcc	23
<210> 68	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 68	
cagtctgccc tgactcagcc tgc	23
<210> 69	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 69	
tcctatgtgc tgactcagcc acc	23
<210> 70	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 70	
tcttctgagc tgactcagga ccc	23
<210> 71	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 71	
cacgttatac tgactcaacc gcc	23
<210> 72	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 72	
caggctgtgc tcactcagcc gtc	23

<210> 73  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 73  
aattttatgc tgactcagcc cca

23

<210> 74  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 74

Ser Ser Ser Ile Leu Cys Ser Pro Leu Pro Ser Leu Ser Leu Ser Val  
1 5 10 15

<210> 75  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 75  
ccttccagat ccacctgaac a

21

<210> 76  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 76  
gacccctgcca ccatgctagt taa

23

<210> 77  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 77  
ctggtctcag aaatattcgt tccgttcct

30

<210> 78  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 78  
gcagcagcgc ccgcgagagc tcattccatac tctgcagcc

39

<210> 79  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 79  
gcagcagtcg acgtccacgt agagtttccg cgtgg 35

<210> 80  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 80  
gcagcagcgg ccgcatgaca actcttggtc ctgcaaccc 39

<210> 81  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 81  
gcagcagtcg acacgagaaa caaaatttat ggcagc 36

35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000  
1001  
1002  
1003  
1004  
1005  
1006  
1007  
1008  
1009  
1010  
1011  
1012  
1013  
1014  
1015  
1016  
1017  
1018  
1019  
1020  
1021  
1022  
1023  
1024  
1025  
1026  
1027  
1028  
1029  
1030  
1031  
1032  
1033  
1034  
1035  
1036  
1037  
1038  
1039  
1040  
1041  
1042  
1043  
1044  
1045  
1046  
1047  
1048  
1049  
1050  
1051  
1052  
1053  
1054  
1055  
1056  
1057  
1058  
1059  
1060  
1061  
1062  
1063  
1064  
1065  
1066  
1067  
1068  
1069  
1070  
1071  
1072  
1073  
1074  
1075  
1076  
1077  
1078  
1079  
1080  
1081  
1082  
1083  
1084  
1085  
1086  
1087  
1088  
1089  
1090  
1091  
1092  
1093  
1094  
1095  
1096  
1097  
1098  
1099  
1100  
1101  
1102  
1103  
1104  
1105  
1106  
1107  
1108  
1109  
1110  
1111  
1112  
1113  
1114  
1115  
1116  
1117  
1118  
1119  
1120  
1121  
1122  
1123  
1124  
1125  
1126  
1127  
1128  
1129  
1130  
1131  
1132  
1133  
1134  
1135  
1136  
1137  
1138  
1139  
1140  
1141  
1142  
1143  
1144  
1145  
1146  
1147  
1148  
1149  
1150  
1151  
1152  
1153  
1154  
1155  
1156  
1157  
1158  
1159  
1160  
1161  
1162  
1163  
1164  
1165  
1166  
1167  
1168  
1169  
1170  
1171  
1172  
1173  
1174  
1175  
1176  
1177  
1178  
1179  
1180  
1181  
1182  
1183  
1184  
1185  
1186  
1187  
1188  
1189  
1190  
1191  
1192  
1193  
1194  
1195  
1196  
1197  
1198  
1199  
1200  
1201  
1202  
1203  
1204  
1205  
1206  
1207  
1208  
1209  
1210  
1211  
1212  
1213  
1214  
1215  
1216  
1217  
1218  
1219  
1220  
1221  
1222  
1223  
1224  
1225  
1226  
1227  
1228  
1229  
1230  
1231  
1232  
1233  
1234  
1235  
1236  
1237  
1238  
1239  
1240  
1241  
1242  
1243  
1244  
1245  
1246  
1247  
1248  
1249  
1250  
1251  
1252  
1253  
1254  
1255  
1256  
1257  
1258  
1259  
1260  
1261  
1262  
1263  
1264  
1265  
1266  
1267  
1268  
1269  
1270  
1271  
1272  
1273  
1274  
1275  
1276  
1277  
1278  
1279  
1280  
1281  
1282  
1283  
1284  
1285  
1286  
1287  
1288  
1289  
1290  
1291  
1292  
1293  
1294  
1295  
1296  
1297  
1298  
1299  
1300  
1301  
1302  
1303  
1304  
1305  
1306  
1307  
1308  
1309  
1310  
1311  
1312  
1313  
1314  
1315  
1316  
1317  
1318  
1319  
1320  
1321  
1322  
1323  
1324  
1325  
1326  
1327  
1328  
1329  
1330  
1331  
1332  
1333  
1334  
1335  
1336  
1337  
1338  
1339  
1340  
1341  
1342  
1343  
1344  
1345  
1346  
1347  
1348  
1349  
1350  
1351  
1352  
1353  
1354  
1355  
1356  
1357  
1358  
1359  
1360  
1361  
1362  
1363  
1364  
1365  
1366  
1367  
1368  
1369  
1370  
1371  
1372  
1373  
1374  
1375  
1376  
1377  
1378  
1379  
1380  
1381  
1382  
1383  
1384  
1385  
1386  
1387  
1388  
1389  
1390  
1391  
1392  
1393  
1394  
1395  
1396  
1397  
1398  
1399  
1400  
1401  
1402  
1403  
1404  
1405  
1406  
1407  
1408  
1409  
1410  
1411  
1412  
1413  
1414  
1415  
1416  
1417  
1418  
1419  
1420  
1421  
1422  
1423  
1424  
1425  
1426  
1427  
1428  
1429  
1430  
1431  
1432  
1433  
1434  
1435  
1436  
1437  
1438  
1439  
1440  
1441  
1442  
1443  
1444  
1445  
1446  
1447  
1448  
1449  
1450  
1451  
1452  
1453  
1454  
1455  
1456  
1457  
1458  
1459  
1460  
1461  
1462  
1463  
1464  
1465  
1466  
1467  
1468  
1469  
1470  
1471  
1472  
1473  
1474  
1475  
1476  
1477  
1478  
1479  
1480  
1481  
1482  
1483  
1484  
1485  
1486  
1487  
1488  
1489  
1490  
1491  
1492  
1493  
1494  
1495  
1496  
1497  
1498  
1499  
1500  
1501  
1502  
1503  
1504  
1505  
1506  
1507  
1508  
1509  
1510  
1511  
1512  
1513  
1514  
1515  
1516  
1517  
1518  
1519  
1520  
1521  
1522  
1523  
1524  
1525  
1526  
1527  
1528  
1529  
1530  
1531  
1532  
1533  
1534  
1535  
1536  
1537  
1538  
1539  
1540  
1541  
1542  
1543  
1544  
1545  
1546  
1547  
1548  
1549  
1550  
1551  
1552  
1553  
1554  
1555  
1556  
1557  
1558  
1559  
1560  
1561  
1562  
1563  
1564  
1565  
1566  
1567  
1568  
1569  
1570  
1571  
1572  
1573  
1574  
1575  
1576  
1577  
1578  
1579  
1580  
1581  
1582  
1583  
1584  
1585  
1586  
1587  
1588  
1589  
1590  
1591  
1592  
1593  
1594  
1595  
1596  
1597  
1598  
1599  
1600  
1601  
1602  
1603  
1604  
1605  
1606  
1607  
1608  
1609  
1610  
1611  
1612  
1613  
1614  
1615  
1616  
1617  
1618  
1619  
1620  
1621  
1622  
1623  
1624  
1625  
1626  
1627  
1628  
1629  
1630  
1631  
1632  
1633  
1634  
1635  
1636  
1637  
1638  
1639  
1640  
1641  
1642  
1643  
1644  
1645  
1646  
1647  
1648  
1649  
1650  
1651  
1652  
1653  
1654  
1655  
1656  
1657  
1658  
1659  
1660  
1661  
1662  
1663  
1664  
1665  
1666  
1667  
1668  
1669  
1670  
1671  
1672  
1673  
1674  
1675  
1676  
1677  
1678  
1679  
1680  
1681  
1682  
1683  
1684  
1685  
1686  
1687  
1688  
1689  
1690  
1691  
1692  
1693  
1694  
1695  
1696  
1697  
1698  
1699  
1700  
1701  
1702  
1703  
1704  
1705  
1706  
1707  
1708  
1709  
1710  
1711  
1712  
1713  
1714  
1715  
1716  
1717  
1718  
1719  
1720  
1721  
1722  
1723  
1724  
1725  
1726  
1727  
1728  
1729  
1730  
1731  
1732  
1733  
1734  
1735  
1736  
1737  
1738  
1739  
1740  
1741  
1742  
1743  
1744  
1745  
1746  
1747  
1748  
1749  
1750  
1751  
1752  
1753  
1754  
1755  
1756  
1757  
1758  
1759  
1760  
1761  
1762  
1763  
1764  
1765  
1766  
1767  
1768  
1769  
1770  
1771  
1772  
1773  
1774  
1775  
1776  
1777  
1778  
1779  
1780  
1781  
1782  
1783  
1784  
1785  
1786  
1787  
1788  
1789  
1790  
1791  
1792  
1793  
1794  
1795  
1796  
1797  
1798  
1799  
1800  
1801  
1802  
1803  
1804  
1805  
1806  
1807  
1808  
1809  
1810  
1811  
1812  
1813  
1814  
1815  
1816  
1817  
1818  
1819  
1820  
1821  
1822  
1823  
1824  
1825  
1826  
1827  
1828  
1829  
1830  
1831  
1832  
1833  
1834  
1835  
1836  
1837  
1838  
1839  
1840  
1841  
1842  
1843  
1844  
1845  
1846  
1847  
1848  
1849  
1850  
1851  
1852  
1853  
1854  
1855  
1856  
1857  
1858  
1859  
1860  
1861  
1862  
1863  
1864  
1865  
1866  
1867  
1868  
1869  
1870  
1871  
1872  
1873  
1874  
1875  
1876  
1877  
1878  
1879  
1880  
1881  
1882  
1883  
1884  
1885  
1886  
1887  
1888  
1889  
1890  
1891  
1892  
1893  
1894  
1895  
1896  
1897  
1898  
1899  
1900  
1901  
1902  
1903  
1904  
1905  
1906  
1907  
1908  
1909  
1910  
1911  
1912  
1913  
1914  
1915  
1916  
1917  
1918  
1919  
1920  
1921  
1922  
1923  
1924  
1925  
1926  
1927  
1928  
1929  
1930  
1931  
1932  
1933  
1934  
1935  
1936  
1937  
1938  
1939  
1940  
1941  
1942  
1943  
1944  
1945  
1946  
1947  
1948  
1949  
1950  
1951  
1952  
1953  
1954  
1955  
1956  
1957  
1958  
1959  
1960  
1961  
1962  
1963  
1964  
1965  
1966  
1967  
1968  
1969  
1970  
1971  
1972  
1973  
1974  
1975  
1976  
1977  
1978  
1979  
1980  
1981  
1982  
1983  
1984  
1985  
1986  
1987  
1988  
1989  
1990  
1991  
1992  
1993  
1994  
1995  
1996  
1997  
1998  
1999  
2000  
2001  
2002  
2003  
2004  
2005  
2006  
2007  
2008  
2009  
2010  
2011  
2012  
2013  
2014  
2015  
2016  
2017  
2018  
2019  
2020  
2021  
2022  
2023  
2024  
2025  
2026  
2027  
2028  
2029  
2030  
2031  
2032  
2033  
2034  
2035  
2036  
2037  
2038  
2039  
2040  
2041  
2042  
2043  
2044  
2045  
2046  
2047  
2048  
2049  
2050  
2051  
2052  
2053  
2054  
2055  
2056  
2057  
2058  
2059  
2060  
2061  
2062  
2063  
2064  
2065  
2066  
2067  
2068  
2069  
2070  
2071  
2072  
2073  
2074  
2075  
2076  
2077  
2078  
2079  
2080  
2081  
2082  
2083  
2084  
2085  
2086  
2087  
2088  
2089  
2090  
2091  
2092  
2093  
2094  
2095  
2096  
2097  
2098  
2099  
2100  
2101  
2102  
2103  
2104  
2105  
2106  
2107  
2108  
2109  
2110  
2111  
2112  
2113  
2114  
2115  
2116  
2117  
2118  
2119  
2120  
2121  
2122  
2123  
2124  
2125  
2126  
2127  
2128  
2129  
2130  
2131  
2132  
2133  
2134  
2135  
2136  
2137  
2138  
2139  
2140  
2141  
2142  
2143  
2144  
2145  
2146  
2147  
2148  
2149  
2150  
2151  
2152  
2153  
2154  
2155  
2156  
2157  
2158  
2159  
2160  
2161  
2162  
2163  
2164  
2165  
2166  
2167  
2168  
2169  
2170  
2171  
2172  
2173  
2174  
2175  
2176  
2177  
2178  
2179  
2180  
2181  
2182  
2183  
2184  
2185  
2186  
2187  
2188  
2189  
2190  
2191  
2192  
2